

09/446415

420 Rec'd PCT/PTO 20 DEC 1999.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Beamer, Lesa J., Carroll, Stephen F., Eisenber, David
- (ii) TITLE OF INVENTION: Bactericidal/Permeability-Increasing Protein: Crystallization, X-Ray Diffraction, Three-Dimensional Structure Determination, Rational Drug Design and Molecular Modeling of Related Proteins
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: McAndrews, Held & Malloy
 - (B) STREET: 500 West Madison, 34th Floor
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60661
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: McNicholas, Janet M.
 - (B) REGISTRATION NUMBER: 32,918
 - (C) REFERENCE/DOCKET NUMBER: 11034US01;100-248
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 312/707-8889
 - (B) TELEFAX: 312/707-9155
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1813 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

006720"STH9460

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 31..1491

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 124..1491

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION: "rBPI"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGGCCTTGA GGTTTTGGCA GCTCTGGAGG ATG AGA GAG AAC ATG GCC AGG GGC	54
Met Arg Glu Asn Met Ala Arg Gly	
-31 -30 -25	
CCT TGC AAC GCG CCG AGA TGG GTG TCC CTG ATG GTG CTC GTC GCC ATA	102
Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile	
-20 -15 -10	
GGC ACC GCC GTG ACA GCG GCC GTC AAC CCT GGC GTC GTG GTC AGG ATC	150
Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile	
-5 1 5	
TCC CAG AAG GGC CTG GAC TAC GCC AGC CAG CAG GGG ACG GCC GCT CTG	198
Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu	
10 15 20 25	
CAG AAG GAG CTG AAG AGG ATC AAG ATT CCT GAC TAC TCA GAC AGC TTT	246
Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe	
30 35 40	
AAG ATC AAG CAT CTT GGG AAG GGG CAT TAT AGC TTC TAC AGC ATG GAC	294
Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp	
45 50 55	
ATC CGT GAA TTC CAG CTT CCC AGT TCC CAG ATA AGC ATG GTG CCC AAT	342
Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn	
60 65 70	
GTG GGC CTT AAG TTC TCC ATC AGC AAC GCC AAT ATC AAG ATC AGC GGC	390
Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly	
75 80 85	
AAA TGG AAG GCA CAA AAG AGA TTC TTA AAA ATG AGC GGC AAT TTT GAC	438
Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp	
90 95 100 105	
CTG AGC ATA GAA GGC ATG TCC ATT TCG GCT GAT CTG AAG CTG GGC AGT	486
Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser	
110 115 120	

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AAC	CCC	ACG	TCA	GGC	AAG	CCC	ACC	ATC	ACC	TGC	TCC	AGC	TGC	AGC	AGC	534
Asn	Pro	Thr	Ser	Gly	Lys	Pro	Thr	Ile	Thr	Cys	Ser	Ser	Cys	Ser	Ser	
			125					130					135			
CAC	ATC	AAC	AGT	GTC	CAC	GTG	CAC	ATC	TCA	AAG	AGC	AAA	GTC	GGG	TGG	582
His	Ile	Asn	Ser	Val	His	Val	His	Ile	Ser	Lys	Ser	Lys	Val	Gly	Trp	
		140					145					150				
CTG	ATC	CAA	CTC	TTC	CAC	AAA	AAA	ATT	GAG	TCT	GCG	CTT	CGA	AAC	AAG	630
Leu	Ile	Gln	Leu	Phe	His	Lys	Lys	Ile	Glu	Ser	Ala	Leu	Arg	Asn	Lys	
	155					160					165					
ATG	AAC	AGC	CAG	GTC	TGC	GAG	AAA	GTG	ACC	AAT	TCT	GTA	TCC	TCC	AAG	678
Met	Asn	Ser	Gln	Val	Cys	Glu	Lys	Val	Thr	Asn	Ser	Val	Ser	Ser	Lys	
170					175					180					185	
CTG	CAA	CCT	TAT	TTC	CAG	ACT	CTG	CCA	GTA	ATG	ACC	AAA	ATA	GAT	TCT	726
Leu	Gln	Pro	Tyr	Phe	Gln	Thr	Leu	Pro	Val	Met	Thr	Lys	Ile	Asp	Ser	
				190					195					200		
GTG	GCT	GGA	ATC	AAC	TAT	GGT	CTG	GTG	GCA	CCT	CCA	GCA	ACC	ACG	GCT	774
Val	Ala	Gly	Ile	Asn	Tyr	Gly	Leu	Val	Ala	Pro	Pro	Ala	Thr	Thr	Ala	
			205					210					215			
GAG	ACC	CTG	GAT	GTA	CAG	ATG	AAG	GGG	GAG	TTT	TAC	AGT	GAG	AAC	CAC	822
Glu	Thr	Leu	Asp	Val	Gln	Met	Lys	Gly	Glu	Phe	Tyr	Ser	Glu	Asn	His	
		220					225					230				
CAC	AAT	CCA	CCT	CCC	TTT	GCT	CCA	CCA	GTG	ATG	GAG	TTT	CCC	GCT	GCC	870
His	Asn	Pro	Pro	Pro	Phe	Ala	Pro	Pro	Val	Met	Glu	Phe	Pro	Ala	Ala	
	235					240					245					
CAT	GAC	CGC	ATG	GTA	TAC	CTG	GGC	CTC	TCA	GAC	TAC	TTC	TTC	AAC	ACA	918
His	Asp	Arg	Met	Val	Tyr	Leu	Gly	Leu	Ser	Asp	Tyr	Phe	Phe	Asn	Thr	
250					255					260					265	
GCC	GGG	CTT	GTA	TAC	CAA	GAG	GCT	GGG	GTC	TTG	AAG	ATG	ACC	CTT	AGA	966
Ala	Gly	Leu	Val	Tyr	Gln	Glu	Ala	Gly	Val	Leu	Lys	Met	Thr	Leu	Arg	
			270					275						280		
GAT	GAC	ATG	ATT	CCA	AAG	GAG	TCC	AAA	TTT	CGA	CTG	ACA	ACC	AAG	TTC	1014
Asp	Asp	Met	Ile	Pro	Lys	Glu	Ser	Lys	Phe	Arg	Leu	Thr	Thr	Lys	Phe	
			285					290					295			
TTT	GGA	ACC	TTC	CTA	CCT	GAG	GTG	GCC	AAG	AAG	TTT	CCC	AAC	ATG	AAG	1062
Phe	Gly	Thr	Phe	Leu	Pro	Glu	Val	Ala	Lys	Lys	Phe	Pro	Asn	Met	Lys	
	300						305					310				
ATA	CAG	ATC	CAT	GTC	TCA	GCC	TCC	ACC	CCG	CCA	CAC	CTG	TCT	GTG	CAG	1110
Ile	Gln	Ile	His	Val	Ser	Ala	Ser	Thr	Pro	Pro	His	Leu	Ser	Val	Gln	
	315					320					325					
CCC	ACC	GGC	CTT	ACC	TTC	TAC	CCT	GCC	GTG	GAT	GTC	CAG	GCC	TTT	GCC	1158
Pro	Thr	Gly	Leu	Thr	Phe	Tyr	Pro	Ala	Val	Asp	Val	Gln	Ala	Phe	Ala	
330					335					340					345	

GTC CTC CCC AAC TCC TCC CTG GCT TCC CTC TTC CTG ATT GGC ATG CAC	1206
Val Leu Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His	
350 355 360	
ACA ACT GGT TCC ATG GAG GTC AGC GCC GAG TCC AAC AGG CTT GTT GGA	1254
Thr Thr Gly Ser Met Glu Val Ser Ala Glu Ser Asn Arg Leu Val Gly	
365 370 375	
GAG CTC AAG CTG GAT AGG CTG CTC CTG GAA CTG AAG CAC TCA AAT ATT	1302
Glu Leu Lys Leu Asp Arg Leu Leu Glu Leu Lys His Ser Asn Ile	
380 385 390	
GGC CCC TTC CCG GTT GAA TTG CTG CAG GAT ATC ATG AAC TAC ATT GTA	1350
Gly Pro Phe Pro Val Glu Leu Leu Gln Asp Ile Met Asn Tyr Ile Val	
395 400 405	
CCC ATT CTT GTG CTG CCC AGG GTT AAC GAG AAA CTA CAG AAA GGC TTC	1398
Pro Ile Leu Val Leu Pro Arg Val Asn Glu Lys Leu Gln Lys Gly Phe	
410 415 420 425	
CCT CTC CCG ACG CCG GCC AGA GTC CAG CTC TAC AAC GTA GTG CTT CAG	1446
Pro Leu Pro Thr Pro Ala Arg Val Gln Leu Tyr Asn Val Val Leu Gln	
430 435 440	
CCT CAC CAG AAC TTC CTG CTG TTC GGT GCA GAC GTT GTC TAT AAA	1491
Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys	
445 450 455	
TGAAGGCACC AGGGGTGCCG GGGGCTGTCA GCCGCACCTG TTCCTGATGG GCTGTGGGGC	1551
ACCGGCTGCC TTTCCCCAGG GAATCCTCTC CAGATCTTAA CCAAGAGCCC CTTGCAAACT	1611
TCTTCGACTC AGATTACAGAA ATGATCTAAA CACGAGGAAA CATTATTCAT TGGAAAAGTG	1671
CATGGTGTGT ATTTTAGGGA TTATGAGCTT CTTTCAAGGG CTAAGGCTGC AGAGATATTT	1731
CCTCCAGGAA TCGTGTTTCA ATTGTAACCA AGAAATTTCC ATTTGTGCTT CATGAAAAAA	1791
AACTTCTGGT TTTTTCATG TG	1813

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Glu Asn Met Ala Arg Gly Pro Cys Asn Ala Pro Arg Trp Val
-31 -30 -25 -20
Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val
-15 -10 -5 1

Asn	Pro	Gly	Val	Val	Val	Arg	Ile	Ser	Gln	Lys	Gly	Leu	Asp	Tyr	Ala	
			5					10					15			
Ser	Gln	Gln	Gly	Thr	Ala	Ala	Leu	Gln	Lys	Glu	Leu	Lys	Arg	Ile	Lys	
		20					25					30				
Ile	Pro	Asp	Tyr	Ser	Asp	Ser	Phe	Lys	Ile	Lys	His	Leu	Gly	Lys	Gly	
	35					40					45					
His	Tyr	Ser	Phe	Tyr	Ser	Met	Asp	Ile	Arg	Glu	Phe	Gln	Leu	Pro	Ser	
	50				55					60					65	
Ser	Gln	Ile	Ser	Met	Val	Pro	Asn	Val	Gly	Leu	Lys	Phe	Ser	Ile	Ser	
				70					75					80		
Asn	Ala	Asn	Ile	Lys	Ile	Ser	Gly	Lys	Trp	Lys	Ala	Gln	Lys	Arg	Phe	
			85					90					95			
Leu	Lys	Met	Ser	Gly	Asn	Phe	Asp	Leu	Ser	Ile	Glu	Gly	Met	Ser	Ile	
		100					105					110				
Ser	Ala	Asp	Leu	Lys	Leu	Gly	Ser	Asn	Pro	Thr	Ser	Gly	Lys	Pro	Thr	
	115					120					125					
Ile	Thr	Cys	Ser	Ser	Cys	Ser	Ser	His	Ile	Asn	Ser	Val	His	Val	His	
	130				135					140					145	
Ile	Ser	Lys	Ser	Lys	Val	Gly	Trp	Leu	Ile	Gln	Leu	Phe	His	Lys	Lys	
				150					155					160		
Ile	Glu	Ser	Ala	Leu	Arg	Asn	Lys	Met	Asn	Ser	Gln	Val	Cys	Glu	Lys	
			165					170					175			
Val	Thr	Asn	Ser	Val	Ser	Ser	Lys	Leu	Gln	Pro	Tyr	Phe	Gln	Thr	Leu	
		180					185					190				
Pro	Val	Met	Thr	Lys	Ile	Asp	Ser	Val	Ala	Gly	Ile	Asn	Tyr	Gly	Leu	
		195				200					205					
Val	Ala	Pro	Pro	Ala	Thr	Thr	Ala	Glu	Thr	Leu	Asp	Val	Gln	Met	Lys	
	210				215					220					225	
Gly	Glu	Phe	Tyr	Ser	Glu	Asn	His	His	Asn	Pro	Pro	Pro	Phe	Ala	Pro	
				230					235					240		
Pro	Val	Met	Glu	Phe	Pro	Ala	Ala	His	Asp	Arg	Met	Val	Tyr	Leu	Gly	
			245					250					255			
Leu	Ser	Asp	Tyr	Phe	Phe	Asn	Thr	Ala	Gly	Leu	Val	Tyr	Gln	Glu	Ala	
		260					265					270				
Gly	Val	Leu	Lys	Met	Thr	Leu	Arg	Asp	Asp	Met	Ile	Pro	Lys	Glu	Ser	
	275					280					285					
Lys	Phe	Arg	Leu	Thr	Thr	Lys	Phe	Phe	Gly	Thr	Phe	Leu	Pro	Glu	Val	
	290				295					300					305	

Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
 310 315 320
 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
 325 330 335
 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
 340 345 350
 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
 355 360 365
 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
 370 375 380 385
 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
 390 395 400
 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
 405 410 415
 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
 420 425 430
 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
 435 440 445
 Gly Ala Asp Val Val Tyr Lys
 450 455

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